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FIG. 1

Multiple Alignment:

SPI	SPkinaseinHSDA59H18	MEKPYAFTVHCVKRAARRHRWKWAQVTFWCPEEQCHLWLQTLREMLEKLTSEPKHLLVFI
CA	CAB62977	-----PKHLLVFI
SPI	SPkinaseinHSDA59H18	NPFGGKGQGKRIYERKVAPLFTLASITTDIGNKFFVN YVEVITEHANQAKETLYEINID
CA	CAB62977	NPFGGKGQGKRIYERKVAPLFTLASITTDIGNKFFVN YVEVITEHANQAKETLYEINID
SPI	SPkinaseinHSDA59H18	KYDGI VCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPR A VLVPSSLRIGIIPAGSTDCWCY
CA	CAB62977	KYDGI VCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPR A VLVPSSLRIGIIPAGSTDCWCY
SPI	SPkinaseinHSDA59H18	STVGTSDAETSALHI VVGDSLAMDVSS VHHNSTLLEY SVSLG YGFYGD I IKDSEKKRWL
CA	CAB62977	STVGTSDAETSALHI VVGDSLAMDVSS VHHNSTLLEY SVSLG YGFYGD I IKDSEKKRWL
SPI	SPkinaseinHSDA59H18	GLARYDFSGLKTF LSHHCYEGT VSFLPAQHTVGSPEDRKPCRAGCFVCRQSKQQL EEEQK
CA	CAB62977	GLARYDFSGLKTF LSHHCYEGT VSFLPAQHTVGSPEDRKPCRAGCFVCRQSKQQL EEEQK
SPI	SPkinaseinHSDA59H18	KALYGLEAAEDVEEWQVVC GKFLAINATNMSCACRRSPRGLSPA AHLGDGSSDLILIRKC
CA	CAB62977	KALYGLEAAEDVEEWQVVC GKFLAINATNMSCACRRSPRGLSPA AHLGDGSSDLILIRKC
SPI	SPkinaseinHSDA59H18	SSEFNFLFLIEHTNQDQDFTFVEVYRVKKFQFTSKHMEDESDLKEGGKKRFGHICSS
CA	CAB62977	SSEFNFLFLIEHTNQDQ-----
SPI	SPkinaseinHSDA59H18	HPSCCCTVSNSSWNCDGEVLHSPAIEVRVHCQLVRLFA RGIENPKPDSHS
CA	CAB62977	-----

FIG. 2

Multiple Alignment:

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S2180312      -----
AI237625      -----
SPkinaseinHSDA59H18  PKHLLVF INPFGKGQGR IYERKVAPLFTLASITTD IIGNKFYVNYVEVITEHANQAKE

S2180312      -----
AI237625      -----
SPkinaseinHSDA59H18  TLYEIN I DKYDGI VCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPA

S2180312      -----
AI237625      -----
SPkinaseinHSDA59H18  GSTDCV CYSTVGTSDAETSA LHI VVGDS LAMDVSSVHHNSTLLRYSVSLG YGFYGD I IK

S2180312      -----
AI237625      -----
SPkinaseinHSDA59H18  DSEKKRWLGLARYDFSGLK TFLSHHCYEGTVSFLPAQHTVGS PRDRKPCRAGCFVCRQSK

S2180312      -----
AI237625      -----
SPkinaseinHSDA59H18  QQLEEEQKKALYGLEAAEDV EEWQVVC GKFLA INA INMSCACACRES PR ELSPFAHLGDGSS

S2180312      -----
AI237625      -----
SPkinaseinHSDA59H18  DLILIRKCSRNFLEFLIRHTNQEDQFGFTFVEVYRVKKFQFTSKHVEDDNDLKELEKQ
DLILIRKCSRNFLEFLIRHTNQDQFDFTFVEVYRVKKFQFTSKHVEDDNDLKEGGRK

S2180312      -----
AI237625      -----
SPkinaseinHSDA59H18  KFGKICKDRPSC TCSASRSWN CDGEV MHS PAIEVRVHCQLVLFARGIEEES
KFGQICKDNFP CACPTSRSSWN CDGEVLHSP AIEVRVHCQLVLFARGIEEES
KFGHIC S SHPSCC CTVSNSSWN CDGEVLHSP AIEVRVHCQLVLFARGIEENPKPDSHS

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FIG. 3

SPkinaseinHSDA59H18 -----MEKPY-----AFTVHCVKRAERRWKWAQVT

coorrected_human_sphingosine -----MPPAGGPRGVLPSPC-RVVLVHINFRGGGKALQLFR
AF068748_EXT-2 -----MEPVCPRGLLPSPC-RVVLVHINFPQGGGKALQLFR
Q06147 LYIDYKPHSS-SHLKEE-DDLVEEIKRSYKNTREK-SIFVITINPFGGGKAKKLFM
Q12246 LLIDHVSRSKRANTGEENISSGTVEEIKRSYENSKEN-SILVFINPHGGGKAKKLFM
O14159 CWVDFVNSD-----QFCEYLDVAYKGIKSS-RFVVFINPHGGGKAKKLFM
Q18425 CRSEAEENEQ-----LTSVLSRKPPPPQEQCGNLLVFINPHSSTHSLTFA
SPkinaseinHSDA59H18 FWCPEEQLCH-----LWLQTLREMLEKLTSPK-HLLVFINPHFEGGQGGHRYE

coorrected_human_sphingosine SHVQLAEAEIIFTIMETER-----RNHARELVE--SEELGRWDALVVMGGGL
AF068748_EXT-2 SHVQLAEAEIIFTKLITER-----KNHARELVC--AEELGHWDALAVMSGDGL
Q06147 TKAKELLASRCSEVYVYIKY-----PGHAIEIAK--ENEDDEYTTACAGGDL
Q12246 TKAKELLVESGCKIEATYIKY-----ARHAIDIAK--DIDISYDTTACAGGDL
O14159 KEAEYVSSHSICGVYETER-----KDHAISYAK--NDVGSYDTTISVGGDL
Q18425 NTVGPKLDKSLTRYEVYITG-----PNHARENLMT--KADLGKENGYLEGGDL
SPkinaseinHSDA59H18 RKVAREFTLASITTDIIGNFYVNYVEVITEHANQAKETLYENEDDEYTTISVGGDL

coorrected_human_sphingosine HEVHIGLMEFPD--WETAIQKPCSEAGSGNAEASINHYAFYEQVTNEDLTNTL
AF068748_EXT-2 HEVHIGLMEFPD--WETAIQKPCSEAGSGNAEASINHYAFYEQVTNEDLTNTL
Q06147 HEVHIGLYQSPDH--VKAFFNTIAETPCSGGNAHVSCHWTN-----NPSYSTLLK
Q12246 YEVDIGLYREFDH--VDAFNKIAETPCSGGNAHVSCHWTN-----NPSYAALLK
O14159 HEVHIGLGEEDD--LEAFKPCMCIEGSGNAHVSCHWTN-----NPSYAALLK
Q18425 FEADIGLGEEDA--FRIPTTEPGIESGSGNCLCSLSKYETKMNEKSVMERALEA
SPkinaseinHSDA59H18 SEVHIGLGETQTSAGVDQNHPRAVLYSSLRIKHIPAGSTDCVCYSTVGTSDAETSAH

coorrected_human_sphingosine LCRPVSPNLLSLHTASGLRSIVLSAGGFIADVLCSEHYR-RLGEMEFITLGTFL
AF068748_EXT-2 LCRPVSPNLLSLHTASGLRSIVLSAGGFIADVLCSEHYR-RLGEMEFITLGTFL
Q06147 SIEIRIDLMCCSQPSYAREHPKLSFLSQTGFIADVLCSEHYR-RLGEMEFITLGTFL
Q12246 SIEIRIDLMCCSQPSYMNEWPRLSFLSQTGFIADVLCSEHYR-RLGEMEFITLGTFL
O14159 GRPVSFDLITFEQ---KGKKAIFLTANYGFIADCDICTENWR-RLGEMEFITLGTFL
Q18425 TSPAKAESVALYSKTDNQSYAFSLSGGFIADVLCSEHYR-RLGEMEFITLGTFL
SPkinaseinHSDA59H18 IIVGDSLAMDVSSVHHNSTLLRSIVLSAGGFIADVLCSEHYR-RLGEMEFITLGTFL

coorrected_human_sphingosine AALTYRRELEATLFRVGVF-----ETP-----
AF068748_EXT-2 AALTYRRELEATLFRVGVF-----ETP-----
Q06147 IQKKVPCIEYVVKYAKSKNELNHYLEH-NHGSLEFQHITMNKDNECDNYNYENEYET
Q12246 IQKKVPCIEYVVKYAKSKKELVHFLEN-DH-----NKGCLTFE-PNPSPN
O14159 FQKPDWKSSEMDVVS SDRTEIKHYE--ETP-----
Q18425 CHLESYKRETYRFPYKPKGFHPSNVFSVYE--TTQQRID--
SPkinaseinHSDA59H18 LSHHCYEETYSFLPAQHTVGSPPD-----KRP-----CRAGCFVCR--

coorrected_human_sphingosine -----ASPVVQVQ-----GPYDAHLVPLEEQ--PSHWQVVP--D
AF068748_EXT-2 -----ASTLVQK-----GPYDTHLVPLEEP--PSHWQVVP--D
Q06147 ENEDDEDADADDEDSHLISRDADSSADQ-IKEEDFKIKYPLDEG-IPSDWERLDPNIS
Q12246 SSPDLLSKNNINNSTKDELSNPNFLN-----EDNFKLKYPMTEP-IPSDWERLDPNIS
O14159 -----N-----EAPMSES-----SDSKTVSTSPD--SHLLTTFE--I
Q18425 -DSKVKTNGSVSDSEEETMETKFN-----WTEPDSDETAVG-SDLEETV--I
SPkinaseinHSDA59H18 QSKQLEEEQKKALYGLEAAEDVEWQVVCCKFLAINATNMSCACRRSIRGLSPAARHGD

coorrected_human_sphingosine EDFVYLALLHHSSEMFAAMORCAAVMHLFYVRAGVSAAALRLFLAMEGRHMEY
AF068748_EXT-2 EDFVYLALLHHSSEMFAAMORCAAVMHLFYVRAGVSAAALRLFLAMEGRHMEY
Q06147 NNLFIFYTGKMPYVADTKFFPAALPSDGTMDVITDARTSLTRMAPILLGLDEG--SHV
Q12246 DNLTIFYTGKMPYVADTKFFPAALPACTGLVITDARTSLTRMAPILLGLDEG--SHV
O14159 NDLSIFCAGLIPYVADAKMFAASNDGLDGVVYSKQFKSLSMFTQLDNE--GFY
Q18425 DNFNVIYAVTLVHADGPFAPSKLEENRHSYLWVDIGTRYNIAKYLLAIEHETH
SPkinaseinHSDA59H18 GSSDLIRKCSRNFNLRFLIRHTNQQTDFTFEYVYKKEFQFTSKHMEDESDLKEG

coorrected_human_sphingosine ECPYLYYPPVVAFLIEPKDGKG--VFANDGEMVSAVGGVHNYFWMYSGCVPSPS
AF068748_EXT-2 ECPYLYYPPVVAFLIEPKDGKG--VFANDGEMVSAVGGVHNYFWMYSGCVPSPS
Q06147 DCYLYYPPVVAFLIEPKDGKG--VFANDGEMVSAVGGVHNYFWMYSGCVPSPS
Q12246 LQPEVLSKILAYKEIPKLGNE--LFSVDGEEKFPLPQVEIMPLCKTLR-----
O14159 LEDEVLSKILAYKEIPKLGNE--LFSVDGEEKFPLPQVEIMPLCKTLR-----
Q18425 YSKHLYYKYSRRTFVNTKREYFANDGESYPLPFECRAEKLGTTLSP-----V
SPkinaseinHSDA59H18 DLFYKHEVSSMKLEVISSEGS--HVVLDGEVVDTKTTEWASTKNHISVFSSTA--
GKKRFGHCCSSHPSCCCTVSNSS--SVNCDGEVHSPAIEVRVHCQLVREIFAR-----

coorrected_human_sphingosine WKPQQMPPPEEPL
AF068748_EXT-2 RDSRRGPPPEEP-
Q06147 -NGRYDITDFDSM
Q12246 -NGRYDITEFSM
O14159 AGFQLLDI-----
Q18425
SPkinaseinHSDA59H18 -GIEENPKPDSHS

C1

C2

C3

C4

C5

FIG. 4

PHYLP - Protein Distance Analysis

Sequences analyzed:

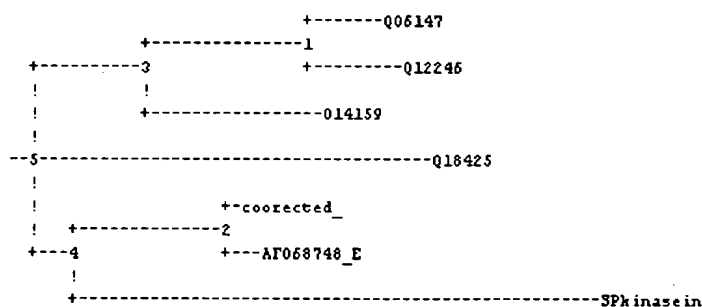
1. SPkinaseinHSDA59H18
2. Q18425
3. O14159
4. Q06147
5. Q12246
6. coorrected_human_sphingosine
7. AF068748_EXT-2

7 Populations

Neighbor-Joining/UPGMA method version 3.572c

Neighbor-joining method

Negative branch lengths allowed



remember: this is an unrooted tree!

Between	And	Length
5	3	1.09970
3	1	1.59865
1	Q06147	0.79847
1	Q12246	1.02742
3	O14159	1.74537
5	Q18425	4.00995
5	4	0.43259
4	2	1.44382
2	coorrected_	0.24774
2	AF068748_E	0.37392
4	SPkinasein	5.26443

FIG. 5

Multiple Alignment:

80432911 SPkinaseinHSDA59H18	AGAPGADAGSVFVSEIIAVEETDVHGKHQSGKWKQIMKPYAFTVHCVKKEA RHRWKWAAQ -----MEKPYAFTVHCVKKEA RHRWKWAAQ
80432911 SPkinaseinHSDA59H18	WTFWCPEEQQLCHLWQLTREMLEKLTSPKHLVFINPFGGKGGKRIYERKVAPLFTLA WTFWCPEEQQLCHLWQLTREMLEKLTSPKHLVFINPFGGKGGKRIYERKVAPLFTLA
80432911 SPkinaseinHSDA59H18	SITTDII-----TEHANQAKETLYEINIDKYDGIWCVGGDGMFSEVLHGLIGR SITTDIIGNKFFWNYVEWTEHANQAKETLYEINIDKYDGIWCVGGDGMFSEVLHGLIGR
80432911 SPkinaseinHSDA59H18	TQESAGVDQNHPR----- TQESAGVDQNHPRAVLPSSLRIGIPAGSTDCVCYSTVGTSDAETSALHIWGD SLAMD
80432911 SPkinaseinHSDA59H18	WSSVHHNSTLLRYSVLLGYGYGDIIDKSEKKRWGLARYDFSGLKTFLSHHCYEGTVS -----
80432911 SPkinaseinHSDA59H18	FLPAQHTVGSPRDEKPCRAGCFVCRQSKQQLLEEQKKALYGLEAAEDVEEWQWVCGKFLA -----
80432911 SPkinaseinHSDA59H18	INATNMSCACRESPRGLSPAHLGDGSSDLILIRKCSRNFLEFLIRHTNQDQDFTFV -----
80432911 SPkinaseinHSDA59H18	EYRVKKEFQFTSKHMEDESDLKEGGKRFEGHICSSHPSCCCTVNSSWNICDGEVLH3PA -----
80432911 SPkinaseinHSDA59H18	IEVEVHCQVRLFARGIEENPEPDSHS -----